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CLARK & ELBING LLP  
101 FEDERAL STREET  
BOSTON, MA 02110

EXAMINER
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MYERS, CARLA J

ART UNIT	PAPER NUMBER
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1634

NOTIFICATION DATE	DELIVERY MODE
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09/23/2008

ELECTRONIC

**Please find below and/or attached an Office communication concerning this application or proceeding.**

The time period for reply, if any, is set in the attached communication.

Notice of the Office communication was sent electronically on above-indicated "Notification Date" to the following e-mail address(es):

patentadministrator@clarkelbing.com

<b>Office Action Summary</b>	<b>Application No.</b> 10/705,531	<b>Applicant(s)</b> LU ET AL.	
	<b>Examiner</b> Carla Myers	<b>Art Unit</b> 1634	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

### Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

### Status

- 1) ☒ Responsive to communication(s) filed on 17 June 2008.
- 2a) ☒ This action is **FINAL**.                      2b) ☐ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

### Disposition of Claims

- 4) ☒ Claim(s) 1-69 is/are pending in the application.
- 4a) Of the above claim(s) 2, 7-46, 48, 49 and 52-69 is/are withdrawn from consideration.
- 5) ☐ Claim(s) \_\_\_\_\_ is/are allowed.
- 6) ☒ Claim(s) 1, 3-6, 47, 50 and 51 is/are rejected.
- 7) ☐ Claim(s) \_\_\_\_\_ is/are objected to.
- 8) ☐ Claim(s) \_\_\_\_\_ are subject to restriction and/or election requirement.

### Application Papers

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☐ The drawing(s) filed on \_\_\_\_\_ is/are: a) ☐ accepted or b) ☐ objected to by the Examiner.  
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).  
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

### Priority under 35 U.S.C. § 119

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All    b) ☐ Some \*    c) ☐ None of:
1. ☐ Certified copies of the priority documents have been received.
2. ☐ Certified copies of the priority documents have been received in Application No. \_\_\_\_\_.
3. ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

\* See the attached detailed Office action for a list of the certified copies not received.

### Attachment(s)

- |  |   |
|--|---|
| 1) <input type="checkbox"/> Notice of References Cited (PTO-892)                     | 4) <input type="checkbox"/> Interview Summary (PTO-413)           |
| 2) <input type="checkbox"/> Notice of Draftsperson's Patent Drawing Review (PTO-948) | Paper No(s)/Mail Date. _____                                      |
| 3) <input type="checkbox"/> Information Disclosure Statement(s) (PTO/SB/08)          | 5) <input type="checkbox"/> Notice of Informal Patent Application |
| Paper No(s)/Mail Date _____  | 6) <input type="checkbox"/> Other: _____                          |

### **DETAILED ACTION**

1. This action is in response to the amendment filed June 17, 2008. Applicant's arguments have been fully considered but are not persuasive to overcome all grounds of rejection. All rejections not reiterated herein are hereby withdrawn. In particular, the rejection of claims 4, 5, 6, and 47 under 35 U.S.C. 112, second paragraph has been obviated by the amendments to these claims. The rejection of claims 1, 3-6, and 47 under 35 U.S.C. 112, first paragraph (written description) is withdrawn since each of these claims requires that the polynucleotide comprises the common structure of the nucleotide sequence of SEQ ID NO: 2.

This action is made final.

2. Claims 1-69 are pending.

Claims 1, 3-6, 47, 50 and 51 have been examined herein.

Claims 2, 7-46, 48, 49, and 52-69 are withdrawn from consideration as being drawn to an invention nonelected with traverse in the reply of May 22, 2006.

### **Maintained Rejections**

#### **Claim Rejections - 35 USC § 112 – Written Description**

3. Claims 50 and 51 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. This is a written description rejection.

This rejection was previously presented in the Office action of December 12, 2007 and has been modified herein to address the amendments to the claims.

In analyzing the claims for compliance with the written description requirements of 35 U.S.C. 112, first paragraph, a determination is made as to whether the specification contains a written description sufficient to show they had possession of the full scope of their claimed invention at the time the application was filed.

The factors to be considered include disclosure of a complete or partial structure, physical and/or chemical properties, functional characteristics, structure/function correlation, and any combination thereof.

Thereby, to ascertain whether the written description requirement is met for a genus claim, it is first determined whether a representative number of species have been described by their complete structure. It is then determined whether a representative number of species have been defined by other identifying characteristics.

In the present application, claims 50 and 51 are drawn to pharmaceutical compositions comprising an antisense oligonucleotide fully complementary to "the mRNA sequence transcribed from a polynucleotide comprising SEQ ID NO: 1." SEQ ID NO: 1 consists of the full length PINX1 cDNA of 1878 nucleotides. The specification (para [0154] teaches that an antisense oligonucleotide may consist of as few as 10bp or may comprise a full length cDNA. The claims define the mRNA in terms of the fact that it is transcribed from SEQ ID NO: 1. However, the claims do not define the complete structure of the mRNA. The claims thereby include antisense oligonucleotides fully

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complementary to both naturally occurring and non-naturally occurring mRNA, including potential splice variants and fragments, that may be transcribed from SEQ ID NO: 1.

The specification teaches the full length cDNA sequence of SEQ ID NO: 1, which encodes for PINX1. The specification teaches that PINX1 binds to Pin2/TFR1 (page 65) and binds to and inhibits telomerase (page 70). The specification also teaches a C-terminal domain of PINX1 (SEQ ID NO: 4) interacts with the telomerase catalytic subunit of hTERT and potentially inhibits its activity in vitro (page 28). SEQ ID NO: 2 consists of a fragment of 1036 of the 1878 nucleotides of SEQ ID NO: 1 and includes the sequence encoding the 75 amino acid sequence of SEQ ID NO: 4.

The specification discloses one full length mRNAs which consist of the RNA sequence of the cDNA of SEQ ID NO: 1. No additional fragments or splice variant mRNAs are disclosed. Presently, there are at least 4 known splice variants of PINX1 (see GeneCard for PINX1 available via url: < [genecards.org/cgi-bin/carddisp.pl?gene=PINX1](http://genecards.org/cgi-bin/carddisp.pl?gene=PINX1)>). However, the specification does not disclose any particular splice variants of SEQ ID NO: 1.

Accordingly, the specification has disclosed only one full length mRNA that is the mRNA sequence of the cDNA of SEQ ID NO: 1 (i.e., the mRNA that consists of SEQ ID NO: 1 with the exception that each thymine is replaced with a uracil) in terms of its complete structure.

No additional members of the claimed genus have been sufficiently described in terms of other relevant identifying characteristics .

It is also noted that possession may not be shown by merely describing how to obtain possession of members of the claimed genus or how to identify their common structural features. See *University of Rochester*, 358 F.3d at 927, 69 USPQ2d at 1895. Thereby, a showing of how to potentially identify and make other PINX1 polynucleotides and mRNAs is not sufficient to establish that Applicant's were in possession of the invention as broadly claimed.

Again, the claimed genus is significantly large includes any naturally occurring or non-naturally occurring mRNA (i.e., splice variant or fragment) that may be transcribed from SEQ ID NO: 1. Thus, the claims encompass naturally occurring and non-naturally occurring homologues, splice, deletion, insertion or substitution variants of PINX1. Yet, the specification teaches only the full length sequence of SEQ ID NO: 1 and a fragment thereof consisting of SEQ ID NO: 2. In the absence of a representative number of species of the claimed genus, there is insufficient descriptive support for the currently claimed genus of PINX1 polynucleotides and mRNAs.

The decisional law in this area has been very consistent. The Federal Circuit in *Lilly*, *Fiers*, *Rochester* and many other cases has determined that the written description issue applies to situations where the definition of the subject matter of the claims fails to provide description commensurate with the genus. The most recent case law directly supports this rejection. As the District Court in *University of Rochester v. G.D. Searle & Co., Inc.* (2003 WL 759719 W.D.N.Y., 2003. March 5, 2003.) noted "In effect, then, the '850 patent claims a method that cannot be practiced until one discovers a compound that was not in the possession of, or known to, the inventors themselves. Putting the

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claimed method into practice awaited someone actually discovering a necessary component of the invention." This is similar to the current situation since the breadth of the current claims encompass PINX1 polynucleotides and mRNAs which the present inventors were not in the possession of, or which were not known to the inventors. As noted in Vas-Cath Inc. v. Mahurkar (19 USPQ2d 1111, CAFC 1991), the Federal Circuit concluded that:

"...applicant must also convey, with reasonable clarity to those skilled in art, that applicant, as of filing date sought, was in possession of invention, with invention being, for purposes of "written description" inquiry, whatever is presently claimed."

Applicant is reminded that *Vas-Cath* makes clear that the written description provision of 35 U.S.C. 112 is severable from its enablement provision.

With respect to the present invention, there is no record or description which would demonstrate conception of any polynucleotides other than those expressly disclosed as comprising SEQ ID NO: 1 or consisting of SEQ ID NO: 2. Therefore, the claims fail to meet the written description requirement because the claims encompass a significantly large genus of polynucleotide sequences which are not described in the specification. Applicants attention is drawn to the Guidelines for the Examination of Patent Applications under 35 U.S.C. 112, ¶ 1 "Written Description" Requirement, Federal Register, Vol. 66, No. 4, pages 1099-1111, Friday January 5, 2001, and particularly Example 14 (<http://www.uspto.gov/web/menu/written.pdf>).

**Response to Remarks:**

In the response, Applicants traverse this rejection. Applicants state that claims 50 and 51 define the mRNA as a sequence transcribed from a polynucleotide comprising

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the sequence of SEQ ID NO: 1. Applicants assert that SEQ ID NO: 1 is a structural feature common to the polynucleotides of claims 50 and 51. Applicants thereby conclude that the complete structure of the mRNA of claims 50 and 51 is clearly defined.

These arguments have been fully considered but are not persuasive. While Applicants argue that the claims are limited to mRNAs defined by the complete sequence of SEQ ID NO: 1, the claims do not include such a limitation. The claims do not define the mRNA as being identical to SEQ ID NO: 1 with the exception that it includes uracil in place of thymine. Rather, the claimed antisense oligonucleotides are defined in terms of being fully complementary to any mRNA transcribed from a polynucleotide comprising SEQ ID NO: 1. Such mRNAs include naturally occurring or artificially derived splice variants of the cDNA of SEQ ID NO: 1. Such antisense oligonucleotides may also be of lengths as short as 10 nucleotides (see para [0154]). Thus, the claimed antisense oligonucleotides are not described in terms of a particular structure - e.g., the nucleotide sequence of the oligonucleotide, the length the oligonucleotide, etc. Accordingly, Applicants arguments are not persuasive because they are not directed to limitations set forth in the claims since the claims are not in fact limited to antisense oligonucleotides that share the common structural feature of SEQ ID NO: 1. As discussed in the above rejection, the disclosure of one full length mRNA that differs from SEQ I D NO: 1 in that it contains uracil in place of thymine is not sufficient to establish possession of the claimed genus of any antisense oligonucleotide



fully complementary to any mRNA that may be naturally or artificially transcribed from the sequence comprising SEQ ID NO: 1. Therefore, the rejection is maintained.

**Claim Rejections - 35 USC § 112 - Enablement**

4. Claims 1, 3-6, 47, 50 and 51 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for isolated polynucleotides comprising SEQ ID NO: 1 and isolated polynucleotides consisting of SEQ ID NO: 2, does not reasonably provide enablement for polynucleotides comprising SEQ ID NO: 2 or antisense polynucleotides fully complementary to any mRNA transcribed from SEQ ID NO: 1. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the invention commensurate in scope with these claims.

The following factors have been considered in formulating this rejection (*In re Wands*, 858F.2d 731, 8 USPQ2d 1400 (Fed. Cir. 1988): the breadth of the claims, the nature of the invention, the state of the prior art, the relative skill of those in the art, the predictability or unpredictability of the art, the amount of direction or guidance presented, the presence or absence of working examples of the invention and the quantity of experimentation necessary.

**Breadth of the Claims:**

Claims 1, 3-6 and 47 are drawn to PINX1 polynucleotides “comprising” the sequence of SEQ ID NO: 1 or 2. SEQ ID NO: 1 consists of the full length PINX1 cDNA of 1878 nucleotides. SEQ ID NO: 2 consists of 1036 nucleotides and encodes a portion of the C-terminal region of PINX1, including the C-terminal 74 amino acids of the PINX1

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protein (SEQ ID NO: 3). In view of the "comprising" language, the claims encompass nucleic acids that contain the 1036 nucleotides of SEQ ID NO: 2 flanked at the 5' end by nucleotides of any length and identity. As such, to the extent that the claims encompass PINX1 polynucleotides comprising SEQ ID NO: 2, the claims define only a portion of PINX1 but do not define the complete structure of PINX1. Accordingly, the claims encompass a very large genus of splice variants, allelic variants, non-naturally occurring variants and homologues of PinX1.

Claims 50 and 51 are drawn to pharmaceutical compositions comprising an antisense oligonucleotide fully complementary to "the mRNA sequence transcribed from a polynucleotide comprising SEQ ID NO: 1." The specification (para [0154]) teaches that an antisense oligonucleotide may consist of as few as 10bp or may comprise a full length cDNA. The claims define the mRNA in terms of the fact that it is transcribed from SEQ ID NO: 1. However, the claims do not define the complete structure of the mRNA. The claims thereby include antisense oligonucleotides fully complementary to both naturally occurring and non-naturally occurring mRNA, including potential splice variants and fragments, that may be transcribed from SEQ ID NO: 1.

Further, claim 4 is drawn to a host cell comprising a DNA vector comprising a polynucleotide comprising SEQ ID NO: 1 or 2. The claim does not recite that the host cell is isolated. Accordingly, the claim reads on host cells present in vivo in a human or other organism produced by the in vivo delivery of a cell or vector.

**Nature of the Invention:**

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The claims are drawn to polynucleotides comprising SEQ ID NO: 1 or 2 or fragments thereof. The invention is in a class of invention which the CAFC has characterized as “the unpredictable arts such as chemistry and biology.” *Mycogen Plant Sci., Inc. v. Monsanto Co.*, 243 F. 3d 1316, 1330 (Fed Cir. 2001).

**Teachings in the Specification and State of the Art:**

The specification teaches the full length cDNA sequence of SEQ ID NO: 1, which encodes for PINX1. The specification teaches that PINX1 binds to Pin2/TFR1 (page 65) and binds to and inhibits telomerase (page 70). The specification also teaches a C-terminal domain of PINX1 (SEQ ID NO: 4) interacts with the telomerase catalytic subunit of hTERT and potentially inhibits its activity in vitro (page 28). SEQ ID NO: 2 consists of a fragment of 1036 of the 1878 nucleotides of SEQ ID NO: 1 and includes the sequence encoding the 75 amino acid sequence of SEQ ID NO: 4.

Regarding claims 50 and 51, the specification discloses full length mRNAs which consist of the RNA sequence of the cDNA of SEQ ID NO: 1. No additional fragments or splice variant mRNAs are disclosed. Presently, there are at least 4 known splice variants of PINX1 (see GeneCard for PINX1 available via url: < [genecards.org/cgi-bin/carddisp.pl?gene=PINX1](http://genecards.org/cgi-bin/carddisp.pl?gene=PINX1)>). However, the specification does not disclosure any particular splice variants of SEQ ID NO: 1.

**The Predictability or Unpredictability of the Art and Degree of Experimentation:**

The claims encompass polynucleotides in which only the 3' region encoding the C-terminal region of the polypeptide are defined. The sequences at the 5' terminus of the polynucleotide are not defined. However, the complete structure of a polypeptide

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determines its binding and inhibitory activity, rather than isolated regions of the polypeptide. Yet, there is no clear disclosure in the specification as to the effect of adding additional amino acids to the N-terminal region of PINX1 will effect the tertiary structure of the protein and thereby its ability to bind to and inhibit telomerase. It is well known in the art that even a single conservative amino acid substitution can adversely effect the proper folding and biological activity of a protein if the amino acids are critical for functional activity. There is no clear disclosure in the specification of the effect of an amino acid substitution, deletion or addition in the N-terminal region on the activity of the proteins encoded by the claimed polynucleotides. While the specification discloses that the polypeptide of SEQ ID NO: 4 binds to and inhibits hTERT, this information is not sufficient to fully characterize the structure-function relationship between all homologues, mutant variants, allelic variants and splice variants of PINX1 and telomerase binding activity. Thereby, it is highly unpredictable as to how the addition of any number of nucleotides of any identity to the 5' region of SEQ ID NO: 2 will effect the overall functional properties of the resulting gene and thus the polypeptide encoded thereby.

It is also unpredictable as to what would be the overall structure of a mRNAs in the genus of mRNAs transcribed from SEQ ID NO: 1. As discussed above, the claims encompass both naturally occurring and artificially generated mRNA splice variants of SEQ ID NO: 1. At present at least 4 splice variants of PINX1 are known. However, the specification does not disclose the existence of such mRNA splice variants or any other splice variants of SEQ ID NO: 1. It is thus highly unpredictable as to what would be the

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overall structure and function of mRNA splice variants naturally or artificially transcribed from SEQ ID NO: 1.

**Amount of Direction or Guidance Provided by the Specification:**

The specification does not provide any specific guidance as to how to predictably make and use nucleic acids comprising SEQ ID NO: 2 flanked by nucleotides of any length and identity. While one could generate a significantly large genus of nucleic acids in which nucleotides of any identity are added to the 5' or 3' terminus of SEQ ID NO: 2 and then assay each of these nucleic acids to try to determine their biological activity, such trial-by-error experimentation is considered to be undue. Providing methods for searching for additional nucleic acids and trying to determine the function of the resulting nucleic acid or trying to establish an association between the nucleic acids and binding to and inhibiting telomerase is not equivalent to teaching how to make and use specific nucleic acids.

Similarly, insufficient guidance is provided in the specification as to how to make and use a representative number of alternatively spliced variants of SEQ ID NO: 1, and the antisense oligonucleotides fully complementary thereto.

**Working Examples:**

Again, the specification teaches only a full length cDNA comprising SEQ ID NO: 1 and one fragment thereof – i.e. a polynucleotide consisting of SEQ ID NO: 2, wherein said polynucleotide encodes for a polypeptide which binds Pin2/TRF-1 and telomerase. The specification does not provide any working examples of how to predictably make and use nucleic acids comprising SEQ ID NO: 2 and including additional nucleotides of

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any length and identity. Further, the specification exemplifies a single mRNA that differs from SEQ ID NO: 1 in that it contains uracil in place of thymine. No additional naturally or non-naturally occurring splice variants of PINX1 mRNAs have been disclosed. Thus, specific working examples are not provided in the specification for a representative number of homologues, splice variants, mutants or allelic variants of PinX1.

**Conclusions:**

Case law has established that “(t)o be enabling, the specification of a patent must teach those skilled in the art how to make and use the full scope of the claimed invention without ‘undue experimentation.’” *In re Wright* 990 F.2d 1557, 1561. *In re Fisher*, 427 F.2d 833, 839, 166 USPQ 18, 24 (CCPA 1970) it was determined that “(t)he scope of the claims must bear a reasonable correlation to the scope of enablement provided by the specification to persons of ordinary skill in the art”. The amount of guidance needed to enable the invention is related to the amount of knowledge in the art as well as the predictability in the art. Furthermore, the Court in *Genetech Inc. v Novo Nordisk* 42 USPQ2d 1001 held that “(I)t is the specification, not the knowledge of one skilled in the art that must supply the novel aspects of the invention in order to constitute adequate enablement”. In the instant case, the claims do not bear a reasonable correlation to the scope of enablement because the specification teaches only SEQ ID NO: 1 and a fragment thereof consisting of SEQ ID NO: 2, whereas the claims encompass a significantly large genus of nucleic acids, in which the overall structural properties and functional properties (with respect to claims 50 and 51) of the nucleic acids are not defined. As set forth above, in view of the unpredictability in the

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art, extensive experimentation would be required to make and use the broadly claimed genus of homologues, mutant, allelic and splice variants of PINX1. Accordingly, although the level of skill in the art of molecular biology is high, given the lack of disclosure in the specification and in the prior art, it would require undue experimentation for one of skill in the art to make and use the broadly claimed invention.

**Response to Remarks:**

In the response, Applicants traversed this rejection.

It is noted that those aspects of the prior rejection over claim 4 as they applied to host cells in vivo have been overcome by the amendment to claim 4 to recite "An isolated host cell."

Regarding claims 1, 3-6 and 47, the response states that the specification teaches the sequence of SEQ ID NO: 2, which is a partial structure of the PINX1 polynucleotides. It is stated that each member of the claimed genus includes SEQ ID NO: 2. Applicants conclude that generation of sequences within the claimed genus would not require undue experimentation.

These arguments have been fully considered but are not persuasive. Applicants do not present any arguments or other evidence to support their conclusion that it would not require undue experimentation to make and use the invention as broadly claimed. While the claims require that the polynucleotides share the common structure of SEQ ID NO: 2, this common structure alone is not sufficient to impart the essential biological activity required by the claims of a polynucleotide encoding a polypeptide that binds to and inhibits telomerase activity. SEQ ID NO: 2 consists of 1036 nucleotides, whereas

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the full length sequence of SEQ ID NO: 1 consists of 1036 nucleotides. Thus, the claims encompass polynucleotides in which only the 3' region encoding the C-terminal region of the polypeptide are defined, whereas the sequences at the 5' terminus of the polynucleotide are not defined. Yet, it is the complete structure of a polypeptide which determines its binding and inhibitory activity, rather than isolated regions of the polypeptide. However, the specification does not provide sufficient guidance as to which or how many amino acids may be added to the N-terminal region of PINX1 without effecting the tertiary structure of the protein and thereby its ability to bind to and inhibit telomerase. There is no clear disclosure in the specification of the effect of an amino acid substitution, deletion or addition in the N-terminal region on the activity of the proteins encoded by the claimed polynucleotides. Thereby, it remains highly unpredictable as to how the addition of any number of nucleotides of any identity to the 5' region of SEQ ID NO: 2 will effect the overall functional properties of the resulting gene and thus the polypeptide encoded thereby.

Regarding claims 50 and 51, the response states that the mRNA is defined as being transcribed from a polynucleotide comprising the sequence of SEQ ID NO: 1. It is stated that SEQ ID NO: 1 is a feature common to the polynucleotides of claims 50 and 51. Applicants state that one of skill in the art would be able to generate mRNA sequences using SEQ ID NO: 1 as a template based on the teachings in the specification. Thereby, Applicants conclude that claims 50 and 51 meet the enablement requirement.



These arguments have also been fully considered but are not persuasive. The claimed antisense oligonucleotides are defined in terms of being fully complementary to any mRNA transcribed from a polynucleotide comprising SEQ ID NO: 1. Such mRNAs include naturally occurring or artificially derived splice variants of the cDNA of SEQ ID NO: 1. Such antisense oligonucleotides may also be of lengths as short as 10 nucleotides (see para [0154]). Thus, the claimed antisense oligonucleotides do not require the common feature of the sequence of SEQ ID NO: 1. As discussed in the above rejection, the specification does not teach how to make and use a representative number of the broadly claimed antisense oligonucleotides. While one of skill in the art may be able to generate a large genus of possible mRNAs from SEQ ID NO: 1, this is not equivalent to teaching how to make and use particular mRNAs for the claimed purpose of generating antisense oligonucleotides to inhibit the expression of PINX1. There is no specific guidance provided in the specification as to what would be the identity of alternatively spliced variants of SEQ ID NO: 1 or how to predictably use antisense oligonucleotides complementary to said mRNAs. Accordingly, it is maintained that given the lack of disclosure in the specification of a representative number of naturally and non-naturally occurring splice variant mRNAs of SEQ ID NO: 1 and given the unpredictability of the art, it would require undue experimentation for one of skill in the art to make and use the invention as broadly claimed.

### **Conclusion**

**THIS ACTION IS MADE FINAL.** Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the mailing date of this final action.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Carla Myers whose telephone number is 571-272-0747. The examiner can normally be reached on Monday-Thursday (6:30-5:00).

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Ram Shukla can be reached on 571-272-0735. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

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Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free). If you would like assistance from a USPTO Customer Service Representative or access to the automated information system, call 800-786-9199 (IN USA OR CANADA) or 571-272-1000.

/Carla Myers/

Primary Examiner, Art Unit 1634